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ABSTRACT OF THE DISCLOSURE NUCLEIC ACID SEQUENCING

A method for determining a target nucleic acid sequence is disclosed, wherein the target nucleic acid sequence is comprised in a preparation comprising a non-target nucleic acid sequence, the target nucleic acid sequence and the non-target nucleic acid sequence each having a first region of common sequence upstream of a first region of dissimilar sequence upstream of a second region of dissimilar sequence. The method comprising:

- (a) centacting the <u>a</u> preparation <u>having a first region of common sequence</u> <u>upstream of a first region of dissimilar sequence upstream of a second region of dissimilar sequence, is <u>contacted</u> with a blocking oligonucleotide complementary to at least a portion of the first region of dissimilar sequence of the non-target nucleic acid sequence, under conditions to hybridise the blocking oligonucleotide thereto[:] and hybridized</u>
- (b) contacting the preparation with a sequencing primer complementary to at least a portion of the first region of common sequence, under conditions to hybridise the primer to the target nucleic acid sequence; and then sequenced
- (c) subjecting the preparation to a sequencing reaction, such that the sequencing reaction proceeds into the second region of dissimilar sequence of the target nucleic acid sequence, thereby determining whereby at least the second region of dissimilar sequence of the target nucleic acid sequence is determined; and wherein the blocking eligonucleotide blocks the sequencing reaction is blocked at least from proceeding into the second region of dissimilar sequence of the non-target nucleic acid sequence.